

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/532,683  
Source: IFP  
Date Processed by STIC: 8/2/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 08/02/2006

PATENT APPLICATION: US/10/532,683

TIME: 08:46:46

Input Set : A:\2005\_0716A Sequence.txt

Output Set: N:\CRF4\08022006\J532683.raw

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3 <110> APPLICANT: Ishihara Sangyo Kaisha, Ltd.
5 <120> TITLE OF INVENTION: Regulation of RAPL-Rap1 Interaction
7 <130> FILE REFERENCE: IS-08PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/532,683
C--> 9 <141> CURRENT FILING DATE: 2005-04-26
9 <150> PRIOR APPLICATION NUMBER: JP 2002-316892
10 <151> PRIOR FILING DATE: 2002-10-30
12 <160> NUMBER OF SEQ ID NOS: 14
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 555
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(555)
24 <223> OTHER INFORMATION: Human Rap1
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29 Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys
30 1          5          10          15
32 tct gct ctg aca gtt cag ttt gtt cag gga att ttt gtt gaa aaa tat      96
33 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr
34          20          25          30
36 gac cca acg ata gaa gat tcc tac aga aag caa gtt gaa gtc gat tgc      144
37 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys
38          35          40          45
40 caa cag tgt atg ctc gaa atc ctg gat act gca ggg aca gag caa ttt      192
41 Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe
42          50          55          60
44 aca gca atg agg gat ttg tat atg aag aac ggc caa ggt ttt gca cta      240
45 Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu
46 65          70          75          80
48 gta tat tct att aca gct cag tcc acg ttt aac gac tta cag gac ctg      288
49 Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu
50          85          90          95
52 agg gaa cag att tta cgg gtt aag gac acg gaa gat gtt cca atg att      336
53 Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile
54          100          105          110
56 ttg gtt ggc aat aaa tgt gac ctg gaa gat gag cga gta gtt ggc aaa      384
57 Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys
58          115          120          125
60 gag cag ggc cag aat tta gca aga cag tgg tgt aac tgt gcc ttt tta      432

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61 Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys Ala Phe Leu
62      130                      135                      140
64 gaa tct tct gca aag tca aag atc aat gtt aat gag ata ttt tat gac      480
65 Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile Phe Tyr Asp
66 145                      150                      155                      160
68 ctg gtc aga cag ata aat agg aaa aca cca gtg gaa aag aag aag cct      528
69 Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys Lys Lys Pro
70                      165                      170                      175
72 aaa aag aaa tca tgt ctg ctg ctc tag      555
73 Lys Lys Lys Ser Cys Leu Leu Leu
74      180
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 184
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2
84 Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys
85 1      5      10      15
88 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr
89      20      25      30
92 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys
93      35      40      45
96 Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe
97      50      55      60
100 Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu
101 65      70      75      80
104 Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu
105      85      90      95
108 Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile
109      100     105     110
112 Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys
113      115     120     125
116 Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys Ala Phe Leu
117      130     135     140
120 Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile Phe Tyr Asp
121 145     150     155     160
124 Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys Lys Lys Pro
125      165     170     175
128 Lys Lys Lys Ser Cys Leu Leu Leu
129      180
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 798
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
137 <220> FEATURE:
138 <221> NAME/KEY: CDS
139 <222> LOCATION: (1)..(798)
140 <223> OTHER INFORMATION: Human RAPL (or Human p30)
143 <400> SEQUENCE: 3

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144	atg	acc	gtg	gac	agc	agc	atg	agc	agt	ggg	tac	tgc	agc	ctg	gac	gag	48
145	Met	Thr	Val	Asp	Ser	Ser	Met	Ser	Ser	Gly	Tyr	Cys	Ser	Leu	Asp	Glu	
146	1				5					10				15			
148	gaa	ctg	gaa	gac	tgc	ttc	ttc	act	gct	aag	act	acc	ttt	ttc	aga	aat	96
149	Glu	Leu	Glu	Asp	Cys	Phe	Phe	Thr	Ala	Lys	Thr	Thr	Phe	Phe	Arg	Asn	
150				20					25				30				
152	gcg	cag	agc	aaa	cat	ctt	tca	aag	aat	gtc	tgt	aaa	cct	gtg	gag	gaa	144
153	Ala	Gln	Ser	Lys	His	Leu	Ser	Lys	Asn	Val	Cys	Lys	Pro	Val	Glu	Glu	
154			35					40					45				
156	aca	cag	cgc	ccg	ccc	aca	ctg	cag	gag	atc	aag	cag	aag	atc	gac	agc	192
157	Thr	Gln	Arg	Pro	Pro	Thr	Leu	Gln	Glu	Ile	Lys	Gln	Lys	Ile	Asp	Ser	
158		50					55					60					
160	tac	aac	acg	cga	gag	aag	aac	tgc	ctg	ggc	atg	aaa	ctg	agt	gaa	gac	240
161	Tyr	Asn	Thr	Arg	Glu	Lys	Asn	Cys	Leu	Gly	Met	Lys	Leu	Ser	Glu	Asp	
162	65				70					75				80			
164	ggc	acc	tac	acg	ggt	ttc	atc	aaa	gtg	cat	ctg	aaa	ctc	cgg	cgg	cct	288
165	Gly	Thr	Tyr	Thr	Gly	Phe	Ile	Lys	Val	His	Leu	Lys	Leu	Arg	Arg	Pro	
166				85					90				95				
168	gtg	acg	gtg	cct	gct	ggg	atc	cgg	ccc	cag	tcc	atc	tat	gat	gcc	atc	336
169	Val	Thr	Val	Pro	Ala	Gly	Ile	Arg	Pro	Gln	Ser	Ile	Tyr	Asp	Ala	Ile	
170			100					105					110				
172	aag	gag	gtg	aac	ctg	gcg	gct	acc	acg	gac	aag	cgg	aca	tcc	ttc	tac	384
173	Lys	Glu	Val	Asn	Leu	Ala	Ala	Thr	Thr	Asp	Lys	Arg	Thr	Ser	Phe	Tyr	
174			115					120					125				
176	ctg	ccc	cta	gat	gcc	atc	aag	cag	ctg	cac	atc	agc	agc	acc	acc	acc	432
177	Leu	Pro	Leu	Asp	Ala	Ile	Lys	Gln	Leu	His	Ile	Ser	Ser	Thr	Thr	Thr	
178		130					135					140					
180	gtc	agt	gag	gtc	atc	cag	ggg	ctg	ctc	aag	aag	ttc	atg	gtt	gtg	gac	480
181	Val	Ser	Glu	Val	Ile	Gln	Gly	Leu	Leu	Lys	Lys	Phe	Met	Val	Val	Asp	
182	145				150					155				160			
184	aat	ccc	cag	aag	ttt	gca	ctt	ttt	aag	cgg	ata	cac	aag	gac	gga	caa	528
185	Asn	Pro	Gln	Lys	Phe	Ala	Leu	Phe	Lys	Arg	Ile	His	Lys	Asp	Gly	Gln	
186				165					170				175				
188	gtg	ctc	ttc	cag	aaa	ctc	tcc	att	gct	gac	cgc	ccc	ctc	tac	ctg	cgc	576
189	Val	Leu	Phe	Gln	Lys	Leu	Ser	Ile	Ala	Asp	Arg	Pro	Leu	Tyr	Leu	Arg	
190			180					185					190				
192	ctg	ctt	gct	ggg	cct	gac	acg	gag	gtc	ctc	agc	ttt	gtg	cta	aag	gag	624
193	Leu	Leu	Ala	Gly	Pro	Asp	Thr	Glu	Val	Leu	Ser	Phe	Val	Leu	Lys	Glu	
194			195					200				205					
196	aat	gaa	act	gga	gag	gta	gag	tgg	gat	gcc	ttc	tcc	atc	cct	gaa	ctt	672
197	Asn	Glu	Thr	Gly	Glu	Val	Glu	Trp	Asp	Ala	Phe	Ser	Ile	Pro	Glu	Leu	
198		210					215					220					
200	cag	aac	ttc	cta	aca	atc	ctg	gaa	aaa	gag	gag	cag	gac	aaa	atc	caa	720
201	Gln	Asn	Phe	Leu	Thr	Ile	Leu	Glu	Lys	Glu	Glu	Gln	Asp	Lys	Ile	Gln	
202	225					230					235				240		
204	caa	gtg	caa	aag	aag	tat	gac	aag	ttt	agg	cag	aaa	ctg	gag	gag	gcc	768
205	Gln	Val	Gln	Lys	Lys	Tyr	Asp	Lys	Phe	Arg	Gln	Lys	Leu	Glu	Glu	Ala	
206				245					250				255				
208	tta	aga	gaa	tcc	cag	ggc	aaa	cct	ggg	taa							798

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209 Leu Arg Glu Ser Gln Gly Lys Pro Gly
210                260                265
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 265
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 4
220 Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu
221 1                5                10                15
224 Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn
225                20                25                30
228 Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu
229                35                40                45
232 Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser
233                50                55                60
236 Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp
237 65                70                75                80
240 Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro
241                85                90                95
244 Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile
245                100               105               110
248 Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr
249                115               120               125
252 Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr
253                130               135               140
256 Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp
257 145               150               155               160
260 Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln
261                165               170               175
264 Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg
265                180               185               190
268 Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu
269                195               200               205
272 Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu
273                210               215               220
276 Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln
277 225               230               235               240
280 Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala
281                245               250               255
284 Leu Arg Glu Ser Gln Gly Lys Pro Gly
285                260                265
288 <210> SEQ ID NO: 5
289 <211> LENGTH: 498
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (1)..(498)
296 <223> OTHER INFORMATION: Dominant-Negative Human RAPL

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Input Set : A:\2005\_0716A Sequence.txt

Output Set: N:\CRF4\08022006\J532683.raw

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299 <400> SEQUENCE: 5
300 gct ggg atc cgg ccc cag tcc atc tat gat gcc atc aag gag gtg aac      48
301 Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn
302 1          5          10          15
304 ctg gcg gct acc acg gac aag cgg aca tcc ttc tac ctg ccc cta gat      96
305 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
306          20          25          30
308 gcc atc aag cag ctg cac atc agc agc acc acc acc gtc agt gag gtc      144
309 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val
310          35          40          45
312 atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac aat ccc cag aag      192
313 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
314          50          55          60
316 ttt gca ctt ttt aag cgg ata cac aag gac gga caa gtg ctc ttc cag      240
317 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
318 65          70          75          80
320 aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc ctg ctt gct ggg      288
321 Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly
322          85          90          95
324 cct gac acg gag gtc ctc agc ttt gtg cta aag gag aat gaa act gga      336
325 Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly
326          100          105          110
328 gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt cag aac ttc cta      384
329 Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu
330          115          120          125
332 aca atc ctg gaa aaa gag gag cag gac aaa atc caa caa gtg caa aag      432
333 Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys
334          130          135          140
336 aag tat gac aag ttt agg cag aaa ctg gag gag gcc tta aga gaa tcc      480
337 Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser
338 145          150          155          160
340 cag ggc aaa cct ggg taa      498
341 Gln Gly Lys Pro Gly
342          165
345 <210> SEQ ID NO: 6
346 <211> LENGTH: 165
347 <212> TYPE: PRT
348 <213> ORGANISM: Homo sapiens
350 <400> SEQUENCE: 6
352 Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn
353 1          5          10          15
356 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
357          20          25          30
360 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val
361          35          40          45
364 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
365          50          55          60
368 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
369 65          70          75          80

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/532,683

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Input Set : A:\2005\_0716A Sequence.txt

Output Set: N:\CRF4\08022006\J532683.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date